

## SEQUENCE LISTING

<110> NARIMATSU, Hisashi et al.

<120> NOVEL N-ACETYLGLUCOSAMINE TRANSFERASE, NUCLEIC ACID ENCODING THE SAME AND USE THEREOF IN DIAGNOSING CANCER AND/OR TUMOR

<130> 0760-0337PUS1

<140> US 10/507,421

<141> 2004-09-13

<150> PCT/JP03/03044

<151> 2003-03-14

<150> JP 2002-70996

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<170> PatentIn 3.2

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Gln His Ala Arg Pro Ile Arg Arg Lys Asp Asn Lys Tyr Tyr Ile Pro	
85 90 95	
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Gly Ala Leu Tyr Gly Lys Ala Ser Tyr Pro Pro Tyr Ala Gly Gly Gly	
100 105 110	
ggc ttc ctc atg gcc ggc agc ctg gcc cgg cgc ctg cac cat gcc tgc	384
Gly Phe Leu Met Ala Gly Ser Leu Ala Arg Arg Leu His His Ala Cys	
115 120 125	
gac acc ctg gag ctc tac ccg atc gac gac gtc ttt ctg ggc atg tgc	432
Asp Thr Leu Glu Leu Tyr Pro Ile Asp Asp Val Phe Leu Gly Met Cys	
130 135 140	
ctg gag gtg ctg ggc gtg cag ccc acg gcc cac gag ggc ttc aag act	480
Leu Glu Val Leu Gly Val Gln Pro Thr Ala His Glu Gly Phe Lys Thr	
145 150 155 160	
ttc ggc atc tcc cgg aac cgc aac agc cgc atg aac aag gag ccg tgc	528
Phe Gly Ile Ser Arg Asn Arg Asn Ser Arg Met Asn Lys Glu Pro Cys	
165 170 175	
ttt ttc cgc gcc atg ctc gtg gtg cac aag ctg ctg ccc cct gag ctg	576
Phe Phe Arg Ala Met Leu Val Val His Lys Leu Leu Pro Pro Glu Leu	
180 185 190	
ctc gcc atg tgg ggg ctg gtg cac agc aat ctc acc tgc tcc cgc aag	624
Leu Ala Met Trp Gly Leu Val His Ser Asn Leu Thr Cys Ser Arg Lys	
195 200 205	
ctc cag gtg ctc tgacccccagc cgggctacta ggacaggcca gggcacttgc	676
Leu Gln Val Leu	
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tcctgagccc ccatggattt ggggctggag ccacagtgcc caggccttagc ctttggtccc	736
caaggggagg tggagggttg aggcctacgt gccactgggt gtgggtgggt gcaggtagcc	796
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tca gcc aat atc aac ttg acc cac cag ccc tgg ttc cag gtc ctg gag 96  
Ser Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu  
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ccg cag ttc cgg cag ttt ctc ttc tac cgc cac tgc cgc tac ttc ccc 144  
Pro Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro  
35 40 45  
atg ctg ctg aac cac ccg gag aag tgc agg ggc gat gtc tac ctg ctg 192  
Met Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu  
50 55 60  
gtg gtt gtc aag tcg gtc atc acg cag cac gac cgc cgc gag gcc atc 240  
Val Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile  
65 70 75 80  
cgc cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc 288  
Arg Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Arg Gly  
85 90 95  
gcc gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag 336  
Ala Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu  
100 105 110  
cgc acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc 384  
Arg Thr His Tyr Gln Gln Leu Ala Tyr Glu Asp Arg Leu Tyr Gly  
115 120 125  
gac atc ctg cag tgg ggc ttt ctc gac acc ttc aac ctg acc ctc 432  
Asp Ile Leu Gln Trp Gly Phe Leu Asp Thr Phe Phe Asn Leu Thr Leu  
130 135 140  
aag gag atc cac ttc ctc aag tgg ctg gac atc tac tgc ccc cac gtc 480  
Lys Glu Ile His Phe Leu Lys Trp Leu Asp Ile Tyr Cys Pro His Val  
145 150 155 160  
ccc ttc att ttc aaa ggc gac gat gac gtc ttc gtc aac ccc acc aac 528  
Pro Phe Ile Phe Lys Gly Asp Asp Asp Val Phe Val Asn Pro Thr Asn  
165 170 175  
ctg cta gaa ttt ctg gct gac cgg cag cca cag gaa aac ctg ttc gtg 576  
Leu Leu Glu Phe Leu Ala Asp Arg Gln Pro Gln Glu Asn Leu Phe Val  
180 185 190  
ggc gat gtc ctg cag cac gct cgg ccc att cgc agg aaa gac aac aaa 624  
Gly Asp Val Leu Gln His Ala Arg Pro Ile Arg Arg Lys Asp Asn Lys  
195 200 205  
tac tac atc ccg ggg gcc ctg tac ggc aag gcc agc tat ccg ccg tat 672  
Tyr Tyr Ile Pro Gly Ala Leu Tyr Gly Lys Ala Ser Tyr Pro Pro Tyr  
210 215 220  
gca ggc ggc ggt ggc ttc ctc atg gcc ggc agc ctg gcc cgg cgc ctg 720  
Ala Gly Gly Gly Phe Leu Met Ala Gly Ser Leu Ala Arg Arg Leu  
225 230 235 240  
cac cat gcc tgc gac acc ctg gag ctc tac ccg atc gac gac gtc ttt 768  
His His Ala Cys Asp Thr Leu Glu Leu Tyr Pro Ile Asp Asp Val Phe  
245 250 255  
ctg ggc atg tgc ctg gag gtg ctg ggc gtg cag ccc acg gcc cac gag 816  
Leu Gly Met Cys Leu Glu Val Leu Gly Val Gln Pro Thr Ala His Glu  
260 265 270

ggc ttc aag act ttc ggc atc tcc cgg aac cgc aac agc cgc atg aac	864
Gly Phe Lys Thr Phe Gly Ile Ser Arg Asn Arg Asn Ser Arg Met Asn	
275 280 285	
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Lys Glu Pro Cys Phe Phe Arg Ala Met Leu Val Val His Lys Leu Leu	
290 295 300	
ccc cct gag ctg ctc gcc atg tgg ggg ctg gtg cac agc aat ctc acc	960
Pro Pro Glu Leu Leu Ala Met Trp Gly Leu Val His Ser Asn Leu Thr	
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Gln Phe Leu Gln Glu Pro Pro Pro Thr Leu Glu Pro Gln Lys Ala	
35 40 45	
Gln Lys Pro Asn Gly Gln Leu Val Asn Pro Asn Asn Phe Trp Lys Asn	
50 55 60	
Pro Lys Asp Val Ala Ala Pro Thr Pro Met Ala Ser Gln Gly Pro Gln	
65 70 75 80	
Ala Trp Asp Val Thr Thr Asn Cys Ser Ala Asn Ile Asn Leu Thr	
85 90 95	
His Gln Pro Trp Phe Gln Val Leu Glu Pro Gln Phe Arg Gln Phe Leu	
100 105 110	
Phe Tyr Arg His Cys Arg Tyr Phe Pro Met Leu Leu Asn His Pro Glu	
115 120 125	
Lys Cys Arg Gly Asp Val Tyr Leu Leu Val Val Val Lys Ser Val Ile	
130 135 140	
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145 150 155 160	
Arg Gln Ser Ala Gly Gly Arg Gly Ala Val Arg Thr Leu Phe Leu	
165 170 175	
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180 185 190	
Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp Ile Leu Gln Trp Gly Phe	
195 200 205	
Leu Asp Thr Phe Phe Asn Leu Thr Leu Lys Glu Ile His Phe Leu Lys	
210 215 220	
Trp Leu Asp Ile Tyr Cys Pro His Val Pro Phe Ile Phe Lys Gly Asp	
225 230 235 240	
Asp Asp Val Phe Val Asn Pro Thr Asn Leu Leu Glu Phe Leu Ala Asp	
245 250 255	
Arg Gln Pro Gln Glu Asn Leu Phe Val Gly Asp Val Leu Gln His Ala	
260 265 270	
Arg Pro Ile Arg Arg Lys Asp Asn Lys Tyr Tyr Ile Pro Gly Ala Leu	
275 280 285	
Tyr Gly Lys Ala Ser Tyr Pro Pro Tyr Ala Gly Gly Gly Phe Leu	
290 295 300	

Met Ala Gly Ser Leu Ala Arg Arg Leu His His Ala Cys Asp Thr Leu  
305 310 315 320  
Glu Leu Tyr Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu Glu Val  
325 330 335  
Leu Gly Val Gln Pro Thr Ala His Glu Gly Phe Lys Thr Phe Gly Ile  
340 345 350  
Ser Arg Asn Arg Asn Ser Arg Met Asn Lys Glu Pro Cys Phe Phe Arg  
355 360 365  
Ala Met Leu Val Val His Lys Leu Leu Pro Pro Glu Leu Leu Ala Met  
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24

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